(1) preparation of one or more fusion genes by cloning the coding sequence of a required passenger in frame with the coding sequence of the transporter domain of the AIDA protein from E.coli or of a variant thereof and of a signal peptide in at least one vector;

(2) where appropriate variation of the passenger peptide or polypeptide by mutagenesis;

(3) introduction of the vector or vectors into host bacteria able to present the passenger or passengers stably on the surface;

(4) expression of the fusion gene or fusion genes in the host bacteria;

(5) cultivation of the bacteria to produce the passenger presented stably exposed on the surface or the passengers presented stably exposed on the surface;

(6) where appropriate selection of the bacteria which carry the passenger or passengers having the required properties on the surface, and

(7) where appropriate characterization of a binding partner for the passenger having the optimal properties.

42. (New) Process according to claim 41, where the process is performed several times.

43. (New) Process according to claim 41, where the passenger protein present in the fusion protein is a peptide or polypeptide having an affinity for a binding partner, or is a ligand, a receptor, an antigen, a toxin-binding protein, a protein with enzymatic activity, a nucleic acid-binding protein, an inhibitor, a protein having chelator properties, an antibody or an antigen-binding domain of an antibody.

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44. (New) Process according to claim 41, where the bacterium which presents a surface-exposed passenger having a required binding affinity is identified by binding to an immobilized or/and labeled binding partner.

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45. (New) Process according to claim 41, where the binding partner is modified so that it can be detected in a second step by a binding partner specific for the modification.

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46. (New) Process according to claim 1, characterized in that passenger proteins or parts thereof are chemically or enzymatically modified on the bacterial surface.

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47. (New) Process according to claim 46, characterized in that the modification is a non-covalent modification.

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48. (New) Process according to claim 46, characterized in that the modification is a covalent modification.

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49. (New) Process according to claim 48, characterized in that the modification is a glycosylation.

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50. (New) Process according to claim 48, characterized in that the modification is a phosphorylation.

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51. (New) Process according to claim 46, characterized in that the modification is a proteolysis.

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52. (New) Process according to claim 51, characterized in that passenger proteins or parts thereof are selectively released from the bacterial surface by intrinsic or externally added proteases.

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53. (New) Process according to claim 52, characterized in that passenger proteins or parts thereof are released by an intrinsic protease of the host cell, in particular OmpT protease, OmpK protease or protease X.

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54. (New) Process according to claim 53, characterized in that passenger proteins or parts thereof are released by an externally added protease, in particular IgA protease, thrombin or factor X.

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55. (New) Recombinant vector on which is located, operatively linked to a promoter, a fused nucleic acid sequence comprising:

(i) a signal peptide-encoding nucleic acid section,

(ii) a nucleic acid section coding for the passenger peptide or/and passenger polypeptide to be presented,

(iii) where appropriate a nucleic acid section coding for a protease recognition site,

(iv) a nucleic acid section coding for a transmembrane linker and

(v) a nucleic acid section coding for the transporter domain of the AIDA protein from E.coli or a variant thereof;

where the nucleic acid section (ii) is heterologous in relation to the nucleic acid section coding for the transporter domain (v).

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56. (New) Recombinant Gram-negative host bacterium, characterized in that it is transformed with a vector according to claim 55.

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57. (New) Recombinant Gram-negative host bacterium which is transformed with a recombinant vector on which is located, operatively linked to a promoter, a fused nucleic acid sequence comprising:

(i) a signal peptide-encoding nucleic acid section,

(ii) a nucleic acid section coding for the passenger peptide or/and passenger polypeptide to be presented,

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(iii) where appropriate a nucleic acid section coding for a protease recognition site,

(iv) a nucleic acid section coding for a transmembrane linker and

(v) a nucleic acid section coding for a transporter domain of an autotransporter;

where the nucleic acid section (ii) is heterologous in relation to the nucleic acid section coding for the transporter domain (v), and where the host bacterium is homologous in relation to the nucleic acid section coding for the transporter domain (v).

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58. (New) Host bacterium according to claim 57, characterized in that it is an E.coli cell.